

0590
0905

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,946

DATE: 10/11/2001

TIME: 10:36:28

Input Set : A:\LEX-0157-USA SEQLIST.txt

Output Set: N:\CRF3\10112001\I819946.raw

ENTERED

4 <110> APPLICANT: Walke, D. Wade
5 Scoville, John
6 Donoho, Gregory
7 Turner, C. Alexander Jr.
8 Friedrich, Glenn
9 Abuin, Alejandro
10 Zambrowicz, Brian
11 Sands, Arthur T.
13 <120> TITLE OF INVENTION: Novel Human 7TM Proteins and Polynucleotides Encoding the
Same
16 <130> FILE REFERENCE: LEX-0157-USA
C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/819,946
C--> 18 <141> CURRENT FILING DATE: 2001-08-27
18 <150> PRIOR APPLICATION NUMBER: US 60/192,978
19 <151> PRIOR FILING DATE: 2000-03-28
21 <160> NUMBER OF SEQ ID NOS: 9
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2526
27 <212> TYPE: DNA
28 <213> ORGANISM: homo sapiens
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57 ccctgtgggg ctgggacctt cctcaacaag agtgacctct acagatgccca gccttgtggg 1620
58 aaagaagagt gggcacctga ggggaagccag acctgcttcc cgcgcactgt ggtgtttttg 1680
59 gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
60 ctgcttggga ctgctggcct gtttgcttg cacctagaca cccctgtggg gaggtcagca 1800
61 gggggccgcc tgtgctttct tatgctgggc tccctggcag caggtagtgg cagcctctat 1860
62 ggcttctttg gggaaacccac aaggcctgcg tgcctgtac gccaggccct ctttgccctt 1920
63 ggtttcacca tcttcctgtc ctgcctgaca gttcgtcat tccaactaat catcatcttc 1980
64 aagttttcca ccaaggtacc tacattctac cagcctggg tccaaaacca cgggtgctggc 2040
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67 acagagacca actccctggg cttcatactg gccttccctt acaatggcct cctctccatc 2220
68 agtgcccttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
69 tgygtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
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71 agcagcggtc tcggtgggta tttctgcct aagtgtacg tgatcctctg ccgccagac 2460
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75 <210> SEQ ID NO: 2

76 <211> LENGTH: 841

77 <212> TYPE: PRT

78 <213> ORGANISM: homo sapiens

80 <400> SEQUENCE: 2

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82 1 5 10 15
83 Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
84 20 25 30
85 Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
86 35 40 45
87 Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
88 50 55 60
89 Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
90 65 70 75 80
91 Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
92 85 90 95
93 Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
94 100 105 110
95 Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
96 115 120 125
97 Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
98 130 135 140
99 Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
100 145 150 155 160
101 Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
102 165 170 175
103 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
104 180 185 190
105 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
106 195 200 205
107 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly

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108      210      215      220
109 Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
110 225      230      235      240
111 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
112      245      250      255
113 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
114      260      265      270
115 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
116      275      280      285
117 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
118      290      295      300
119 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
120 305      310      315      320
121 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
122      325      330      335
123 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys
124      340      345      350
125 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
126      355      360      365
127 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
128      370      375      380
129 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
130 385      390      395      400
131 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
132      405      410      415
133 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
134      420      425      430
135 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
136      435      440      445
137 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
138      450      455      460
139 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
140 465      470      475      480
141 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
142      485      490      495
143 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
144      500      505      510
145 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
146      515      520      525
147 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
148      530      535      540
149 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
150 545      550      555      560
151 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
152      565      570      575
153 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
154      580      585      590
155 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
156      595      600      605

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157 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
158      610                      615                      620
159 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
160 625                      630                      635                      640
161 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
162                      645                      650                      655
163 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
164                      660                      665                      670
165 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
166                      675                      680                      685
167 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
168      690                      695                      700
169 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
170 705                      710                      715                      720
171 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
172                      725                      730                      735
173 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
174                      740                      745                      750
175 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
176                      755                      760                      765
177 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
178      770                      775                      780
179 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
180 785                      790                      795                      800
181 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
182                      805                      810                      815
183 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
184                      820                      825                      830
185 Asp Tyr Thr Arg Arg Cys Gly Ser Thr
186      835                      840

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188 <210> SEQ ID NO: 3

189 <211> LENGTH: 2292

190 <212> TYPE: DNA

191 <213> ORGANISM: homo sapiens

193 <400> SEQUENCE: 3

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196 ctctccctgc cagggcaaca ccacatagag ctccaaggag accttctcca ctattccct      180
197 acggtgctgg cagtgattgg gcctgacagc accaaccgtg ctgccaccac agccgccctg      240
198 ctgagccctt tcctgggtgcc catgattagc tatgcggcca gcagcgagac gctcagcgtg      300
199 aagcggcagt atccctcttt cctgcgcacc atccccaatg acaagtacca ggtggagacc      360
200 atggtgctgc tgctgcagaa gttcgggttg acctggatct ctctggttgg cagcagtgac      420
201 gactatgggc agctaggggt gcaggcactg gagaaccagg cactgggtca ggggatctgc      480
202 attgctttca aggacatcat gcccttctct gcccagggtg gcgatgagag gatgcagtgc      540
203 ctcatgcgcc acctggccca ggccggggcc accgtcgttg ttgttttttc cagccggcag      600
204 ttggccaggg tgtttttcga gtccgtggtg ctgaccaacc tgactggcaa ggtgtgggtc      660
205 gcctcagaag cctgggccct ctccaggcac atcactgggg tgcccgggat ccagcgcatt      720
206 gggatggtgc tgggcgtggc catccagaag agggctgtcc ctggcctgaa ggcgtttgaa      780
207 gaagcctatg cccgggcaga caaggaggcc cctaggcctt gccacaaggg ctccgtggtgc      840

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TIME: 10:36:28

Input Set : A:\LEX-0157-USA SEQLIST.txt

Output Set: N:\CRF3\10112001\I819946.raw

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208 agcagcaatc agctctgcag agaatgccaa gctttcatgr cacacacgat gccaagctc 900
209 aaagccttct ccatgagttc tgcctacaac gcataccggg ctgtgtatgc ggtggcccat 960
210 ggctccacc agctcctggg ctgtgcctct ggagcttggt ccaggggccc agtctacccc 1020
211 tggcagcttt tggagcagat ccacaagggt catttccttc tacacaagga cactgtggcg 1080
212 tttaatgaca acagagatcc cctcagtagc tataacataa ttgcctggga ctggaatgga 1140
213 cccaagtgga ccttcacggt cctcggttcc tccacatggt ctccagttca gctaaacata 1200
214 aatgagacca aaatccagtg gcacggaaa gacaaccagg tgcctaagtc tgtgtgttcc 1260
215 agcgactgtc ttgaagggca ccagcgagtg gttacgggtt tccatcactg ctgctttgag 1320
216 tgtgtgccct gtggggctgg gaccttctc aacaagagtg acctctacag atgccaqcc 1380
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218 tttttggctt tgcgtgagca cacctcttgg gtgctgctgg cagctaacac gctgctgctg 1500
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225 gtggtgtgga cccactgcc tgcaggga taccagcgt tccccatct ggtgatgctt 1920
226 gagtgcacag agaccaactc cctgggcttc atactggcct tccctacaa tggcctcctc 1980
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229 acggccagcg tctacgacgg caagtacctg cctgcggcca acatgatggc tgggctgagc 2160
230 agcctgagca gcggtctcgg tgggtatitt ctgcctaagt gctacgtgat cctctgccgc 2220
231 ccagacctca acagcacaga gcacttcacg gcctccattc aggactacac gaggcgtgc 2280
232 ggctccacct ga 2292

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234 <210> SEQ ID NO: 4

235 <211> LENGTH: 763

236 <212> TYPE: PRT

237 <213> ORGANISM: homo sapiens

239 <400> SEQUENCE: 4

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243 20 25 30
244 Asn Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His
245 35 40 45
246 Ile Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala
247 50 55 60
248 Val Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu
249 65 70 75 80
250 Leu Ser Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu
251 85 90 95
252 Thr Leu Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro
253 100 105 110
254 Asn Asp Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Lys Phe
255 115 120 125
256 Gly Trp Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln
257 130 135 140
258 Leu Gly Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys

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VERIFICATION SUMMARY

DATE: 10/11/2001

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TIME: 10:36:29

Input Set : A:\LEX-0157-USA SEQLIST.txt

Output Set: N:\CRF3\10112001\I819946.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date